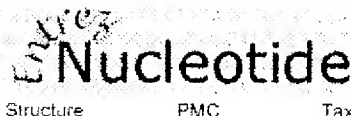


**Exhibit 1: Genbank Accession CP000702**



Search Nucleotide

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Details

Display GenBank(Full) Show 5 Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from 148657 to 149595

Show whole sequence

☐ Reverse complemented strand Features: [

☐ 1: CP000702. Reports *Thermotoga petrophila*...[gi:147734689]

Links

Comment Features Sequence

LOCUS CP000702 939 bp DNA linear BCT 06-DEC-2007

DEFINITION *Thermotoga petrophila* RKU-1, complete genome.

ACCESSION CP000702 REGION: 148657..149595

VERSION CP000702.1 GI:147734689

PROJECT GenomeProject:17089

KEYWORDS .

SOURCE *Thermotoga petrophila* RKU-1

ORGANISM *Thermotoga petrophila* RKU-1

Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

REFERENCE 1 (bases 1 to 939)

AUTHORS Copeland,A., Lucas,S., Lapidus,A., Barry,K., Glavina del Rio,T., Dalin,E., Tice,H., Pitluck,S., Sims,D., Brettin,T., Bruce,D., Detter,J.C., Han,C., Tapia,R., Schmutz,J., Larimer,F., Land,M., Hauser,L., Kyrpides,N., Mikhailova,N., Nelson,K., Gogarten,J.P., Noll,K. and Richardson,P.

TITLE Complete sequence of *Thermotoga petrophila* RKU-1

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 939)

AUTHORS Copeland,A., Lucas,S., Lapidus,A., Barry,K., Glavina del Rio,T., Dalin,E., Tice,H., Pitluck,S., Sims,D., Brettin,T., Bruce,D., Detter,J.C., Han,C., Tapia,R., Schmutz,J., Larimer,F., Land,M., Hauser,L., Kyrpides,N., Mikhailova,N., Nelson,K., Gogarten,J.P., Noll,K. and Richardson,P.

TITLE Direct Submission

JOURNAL Submitted (14-MAY-2007) US DOE Joint Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT URL -- <http://www.jgi.doe.gov>

JGI Project ID: 4002277

Source DNA and bacteria available from Kenneth Noll (kenneth.noll@uconn.edu)

Contacts: Kenneth Noll (kenneth.noll@uconn.edu)

Paul Richardson (microbes@cuba.jgi-psf.org)

Quality assurance done by JGI-Stanford

Annotation done by JGI-ORNL and JGI-PGF

Finishing done by JGI-LANL

Finished microbial genomes have been curated to close all gaps with greater than 98% coverage of at least two independent clones. Each base pair has a minimum q (quality) value of 30 and the total error rate is less than one per 50000.

The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

FEATURES Location/Qualifiers

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